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Title:
Perfect score:
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DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 2000000000
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Match
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Listing first 45 summaries
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1793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13736207 seqs, 6748477542 residues
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   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gaattccctgttgacaatta.....caattactcaatgcccgcgg 1793
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em_gss_hum:*
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AF114216

AQ989631

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AF029514

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AW7103376

AW710318

BE092318

AW948136

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AW948130

AW948130

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AQ329770 nbxb0045P
AF114216 AF114216
AQ989631 Rfc00197
AQ989631 Rfc001897
AQ990982 Rfc01832
AF029514 AF029514
AQ329769 nbxb0045P
AQ110684 mgxb0006L
AW711275 flallne.f
AW711275 flallne.f
AW711819 e6h01ne.f
BE092318 ILZ-BT073
AW948136 RC0-MT001
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		0 0 0 0 0 0 5 5 5 5 5	22.6667777	2.99
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BG912542 BE434941 BI269359 BI269270 BE460888	AV945848 AV944572 AG010512	BM373215 BM443910 BM098909 AQ016380 AV942445	BH390360 BE600147 AI329382 BF484942 BF072824 CNS0091P BF473461	AW948147 AW710710 AW708803 AW714224 AF404216 BG278308 AF114188
	AV945848 AV945848 AV944572 AV944572 AV944572 AV944572 AG010512 Homo sapi	BM373215 EBma04_SQ BM443910 EBem09_SQ BM098909 EBp105_SQ AQ016380 CIT-HSP-2 AV942445 AV942445	ъ	AW948147 RC0-MT001 AW710710 e5f03ne.f AW708803 c9e12ne.f AW714224 h6909ne.f AF408416 AF408416 BG278308 a3d02np.r AF114188 AF114188

## ALIGNMENTS

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REFERENCE
AUTHORS
TITLE
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KEYWORDS
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AQ329770/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ329770
AQ329770.1
GSS.
                                                                                                                                                                                                                      High quality sequence start: 13
High quality sequence stop: 225
Location/Qualifiers
                                                                                                                                                                                                                                                                                 100 Jordan Hall, Clemson, SC 29
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wing RA
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 888),
Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AQ329770 888 bp DNA linear GSS nbxb0045P09r CUGI Rice BAC Library Oryza sativa genomic nbxb0045P09r, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa.
/Clone="hbxb0045903"
/Clone_lib="CUGI Rice BAC Library"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
/hindIII; Rice is one of two most popular grains in the
                                                                                                                          /organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GI:4121620
                                                                                                                                                                                                            . 888
                                                                                                                                                                                                                                                                                                                                                                                      29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence the Rice Genome
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clone
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SOURCE
ORGANISM
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AF114216/c
                                                                                                                     REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    cttgagcaagtacgcgctgtactcccagcacgaagccattcacattgccgcctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGTGCTGTCGAGCGACCTTGGCCGGCTTGGATCGCTTTGCTGCTGGGAACATATGAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tgtgtccgacaccgagctgggccgcgtcggttgccctgttgctgctgggagcacctgtcccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGATCGACAGTCAGAAAACAGCANGNCCGCAGATGGCCCGGAGTCGGCGCGNATCGCCGA 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgcccgctactatgccaactcgctctcgctggacagtgcagagtttcaacgcattgccca
Unpublished (1999)
Contact: McClelland M
Molecular Biology
                                                                                           Wong, R.M.Y. and McCl
                                                                                                                                                                          Salmonella typhimurium.
Salmonella typhimurium
                                                                                                                                                                                                                   AF114216.1
GSS.
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                                                                                                                                                                                                                                                         typhimurium
AF114216
                                                                                                                                      Salmonella.
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                                                                   Sequences of Salmono.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              library from Oryza Sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10,9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening. 18 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carbohydrate. Monocotyledonous rice is a diploid plant (2n-24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of
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and genom
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58.2%;
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..6e-28;
les 173;
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Salmonella
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ORIGIN

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VERSION

COMMENT

/clone\_lib="Photorhabdus

Luminescens

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KEYWORDS
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                                                                                                                                                    Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping
coli K12 genome) please see ffrench-Constant et al. 2000, Nu
                                                                                                                                                                                                                          South Building, Bath | Tel: (44) 1225 826621 Fax: (44) 1225 826779
                                                                                                                                                                                                                                                                 Department of Biology and Biochemistry University of Bath
                                                                                                                                                                                                                                                                                                                                Appl. Env
20378633
                                                                                                                                                                                                                                                                                                                                              ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T Daborn,P.J., Bowen,D. and Blattner,F.R. Agenomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens w14: potential implications for via Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ989631 544 bp DNA linear GSS 14-AUG
Rfc00197 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00197, DNA sequence.
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Class: shotgun
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3099 Science Park Road, San
                                                                                                                      Seq primer: M13 Forward
                                                                                                                                         Acids Res
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Photorhabdus
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                                                                                                     shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mcclelland@lifsci.sdsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequencer"
1 292 c
/db_xref="taxon:29488"
/clone="PLG00197"
                                   /strain="W14"
                                                  organism="Photorhabdus"
                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Salmonella typhimurium LT2, Lambda DASH II"
/note="Vector: Lambda DASH II; sequenced using Li-Cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="45-T7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="LT2"
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85.5%;
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No. 5e
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                                                   luminescens'
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BASE COUNT
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MEDLINE
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Best Local :
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                                                                                                                                                                                                                                                                                                                                           Contact: ffrench-Constant RH
Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Teax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping annotation of identified clones (BLASTX, BLASTN and mapping annotation of identified clones (BLASTX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ990982 655 bp DNA linear GSS Rfc01832 Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens genomic clone PLG01832, DNA seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T Daborn, P.J., Bowen, D. and Blattner, F.R.
Daborn sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for vin Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                       Seq primer: M1:
Class: shotgun
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Photorhabdus luminescens
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/dev_stage="primary phase variant"
/note="Genomic DNA from strain W14 was size
/note="Genomic cloned into M13 Janus."
kb) and then cloned into M13 Janus."
a 108 c 123 g 183 t 1 others
                /dev_stage="primary phase variant"
/note="Genomic DNA from strain W14 was size selected kb) and then cloned into M13 Janus."
kb) and then cloned into M13 Janus."
160 c 170 g 151 t 1 others
                                                                                                      library
                                                                                                                                                    /clone="PLG01832"
                                                                                                                                                                           /db_xref="taxon:29488"
                                                                                                                                                                                             /strain="W14"
                                                                                                                                  /clone_lib="Photorhabdus luminescens strain
                                                                                                                                                                                                                    /organism="Photorhabdus
                                                                                                                                                                                                                                                             Location/Qualifiers
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75.9%;

 Mismatches

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Pred. No. 1.1e-18;
                                                                                                                                                                                                                         Luminescens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perna, N.T.,
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                                                                                                                                  W14
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Query Match

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Score

104;

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RESULT
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AUTHORS
TITLE
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Best Local Similarity
Matches 123; Conserv
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                tgaaacgccgtagcgccgatggtagtgtggggtctcccccatgcgagagtaggggaactgcc 1386
                                                                                                                   AGAATTTGCCTGGCGGCACTAGCGCGGTGGTCCCCACCTGACCCCATGCCGAACTCAGAAG
                                                                                                                                 agagtcgacctgcaggcatgcaagcttgggtcccacctgaccccatgccgaactcagaag 1326
AGGCATCAAATTAGAAGTATGGC
                                                          {\tt TGAAACGCCGTAGCGCCGATGGTAGTGTGGGGGTCT-CCCATGCGAGAGTAGGGAACTGCC}
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typhimurium genomic clone 715-T7, DNA sequence.
AF029514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 1101)
Wong, R. M.-Y., Wong, K. K., Benson, N. R. and McClelland, M. Sample sequencing of a Salmonella typhimurium LT2 lambda comparison to the Escherichia coli K12 genome FEMS Microbiol. Lett. 173 (2), 411-423 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salmonella typhimurium.
Salmonella typhimurium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Molecular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: McClelland M
                                                                                                                                                                                                                                                                   289
                                                                                                                                                                                                                                                                                                                                                                                                                                ey Kimmel Cancer Center
Science Park Road, San Diego,
l: mcclelland@lifsci.sdsu.edu
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    shotgun
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                                                                                                                                                                                                                                                                sequencer"
a 248 c
                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:602"
/clone="715-T7"
                                                                                                                                                                                                                                                                                            /clone_lib="Salmonella typhimurium LT2, Lambda
/note="Vector: Lambda DASH II; sequenced using
                                                                                                                                                                                                                                                                                                                                                        /strain="LT2"
                                                                                                                                                                                                                                                                                                                                                                       /organism="Salmonella
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); Mismatches 50;
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                       753 atctattcggttgaaggccagtgctttaccatcgccgccagcagtgtcgtcacccaggag 812
62
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GTCTACGCGGCCGAGGGACAATGCTTCGTGATCGCGCCCCTGCGGGGTTGTTTCTGCGGAA 121
                                                                                        TCGCTCTACAACGGCAAGGCTTTCGCGCTCGGTCCCGAGCTCAACAATGCCGTCAGCCAG
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Clemson University
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A BAC End Sequencing Framework to
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oryza sativa.
Oryza sativa
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622 bp DNA linear GSS 08-JAN nbxb0045P09f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0045P09f, DNA sequence.
AQ329769
AQ329769
AQ329769.1 GI:4121619
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: TAATACGACTCACTATAGGG
Class: BAC ends
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                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                 112
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Location/Qualifiers
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                      //note="Vector: pBeloBAC11; Site_1: HindIII; Site_2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab_host="E. coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="CUGI Rice BAC Library"
/tissue_type="Leaf"
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/db_xref="taxon:4530"
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/strain="Japonica"
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100 Jordan Hall, Cl
Tel: 864 656 5737
Fax: 864 656 4293
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AQ160684 AQ160684.1 GI:3557673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 580)
Yu,Y., 2hu,H., Boyd,C.A., Gaudette,B., Gayle,A., Kingsbury,R., Phillips,K., Sasinowski,M., Wing,R.A. and Dean,R.A.
A BAC End Sequencing Framework to Sequence the Magnaporthe gri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Magnaporthe grisea
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sor
Sordariomycetes incertae sedis; Magnaporthaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 357.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Dean RA
Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: rdean@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Magnaporthe grisea.
                       132
              containing 9216 clones with an average insert size of 130 kbp was constructed. This library represents greater than 25x genome coverage. High density colony filters are available upon request."
                                                                                                                               note "Vector: pBACWICH; Site_1: HindIII; Site_2: HindIII; Rice blast is one of the most devestating fungal diseases of rice world wide. It is a filamentous ascomycete with a haploid genome (n=7) of approximately 40 Mbp. Rice blast is an important model fungal pathogen for studying numerous aspects of the fungal-host interaction. In order to facilitate genome wide analysis, a BAC library
                                                                                                                                                                                                                                                                                                                                         /clone="mgxb0006L04r"
/clone_lib="CUGI Rice Blast
                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:148305"
                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Magnaporthe grisea"
/strain="70-15"
                                                                                                                                                                                                                                                                                            /tissue_type="Protoplasts"
/lab_host="E. coli DH10B"
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Query Match
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Matches 192; Conserv

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Score 83.6; DB 12; Pred. No. 1e-12; Mismatches

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    189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA clone
AW711275
AW711275.1
                                                                                                                                                                                                                                                                                                                                    Advanced Center for Genome Technology,
620 Parrington Oval, Norman, OK 73019,
Tel: 405 325 4912
Fax: 405 325 7762
                                                                                                                                                                                                                                                                                                                                                                                         Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
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Other_ESTs: flallne.rl
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Two Neurospora crassa EST
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/strain="Strain 30-7 (bd; A)"
/db_xref="taxon:5141"
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Fax: 405 325 7762
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/note="Vector: pBlueScript SK-; Site_1: XbaI; Site_2: EcoRI; See: Bell-Perdersen,D., et al. PNAS 93:13096,1996 5' end of cDNA cloned into XbaI site of pBluescript; 3' end of cDNA cloned into EcoRI site of pBluescript" a 136 c 103 g 85 t
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                                                                                                                                                                                                                                                                                                                                    Department of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklahoma Advanced Center for Genome Technology, University of Oklahoma Advanced Center for Oklahoma (NK 73019, USA)
                                                                                                                                                                                                                                                             Email: broe@ou.edu
We anticipate the future release
Genetics Stock Center
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Fax: 405 325 7762
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/strain="Strain 30-7 (bd; A)"
/db_xref="taxon:5141"
/clone="e6h0lne"
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                                                                                                     /clone_lib="Neurospora crassa e
/tissue_type="tissue harvested
                         ote="Vector: pBlueScript SK-; Site_1: XbaI; Site_2: oRI; See: Bell-Perdersen,D., et al. PNAS 93:13096,1996. end of cDNA cloned into XbaI site of pBluescript; 3'd of cDNA cloned into EcoRI site of pBluescript"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            crassa
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BE092318
BE092318.1 GI:8482770
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1 (bases 1 to 330)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                               Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be from in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=IL2-BT0734-240
400-072-D10&t3=2000-04-24&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer R
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                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BT0734"
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Pred. No. 4.4e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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RCO-мT0013-280300-031-c06 мТ0013
AW948136
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
Project. This entry can be seen in the following URL
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
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300-031-c06&t3=2000-03-28&t4=1)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Similarity 77.98;
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/note="Organ: marrow; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196. 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
                                                                                                                                                                  /clone_lib="MT0013"
/dev_stage="Adult"
                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 8.7e-10;
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                                                                                                                                                                                                                                                                                                                                                                                     This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
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                                                                                                                                                                                                                                                                                                                                                  (http://www.ludwig.org.br/scripts/gethtml2.pl7t1=&t2=RC0-MT0013-280 300-031-b07&t3-2000-03-28&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G.
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1 (bases 1 to 707)
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                                                                                                                                                                                                                                                                                                                                                                                                                              Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: +55-11-2704922
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                  168
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        /note="Organ: marrow; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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a 163 c 195 g
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Pred. No. 2.1e-09;
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                      1289 agcttgggtcccacctgaccccatgccgaactcagaagtgaaacgccgtagcgccgatgg 1348
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561 AGCATTGGAACCACCTGATCCCGAACTCAGCAGTGAAACGATGGATCGCCGATGG
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1 (bases 1 to 708)

Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=6t2=RCO-MT0013-280
300-031-e04xt3=2000-03-28xt4=1)
Seq.primer: puc 18 forward
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Ludwig Institute for Cancer Re
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                                                                                                            Similarity
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/db_xref="taxon:9606"
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ismatches 23;
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AGCATTGGAACCACCTGATCCCATCCCGAACTCAGCAGTGAAACGATGCATCGCCGATGG 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., debliveira,P.S., Bucher,P., Jongeneal,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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171 c 206 g 1
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